

SEQUENCE LISTING

<110> Potter, Andrew A.
Perez-Casal, Jose
Fontaine, Michael

<120> IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
AGAINST STREPTOCOCCUS INFECTION

<130> 9000-0057

<140> 09/878,766

<141> 2001-06-11

<160> 22

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<212> DNA

<213> Streptococcus dysgalactiae

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<221> CDS

<222> (1)..(1011)

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1 5 10 15

48

gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

96

aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tac gat
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

144

aca act caa gga cgt ttt gac gga act gtt gaa gtt aaa gaa ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
50 55 60	
ttt gaa gta aac gga aac ttc atc aaa gtt tct gct gaa cgt gat cca	240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro	
65 70 75 80	
gaa aac atc gac tgg gca act gac ggt gtt gaa atc gtt ctg gaa gca	288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct	336
Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala	
100 105 110	
aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act	528
Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr	
165 170 175	
aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	
cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt	768
Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val	
245 250 255	

gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt 816
 Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
 260 265 270

 tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac 864
 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
 275 280 285

 ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga 912
 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
 290 295 300

 tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac 960
 Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
 305 310 315 320

 act gct caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa 1008
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 taa 1011

<210> 12
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 <212> PRT
 <213> Streptococcus dysgalactiae

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 20 25 30

 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
 35 40 45

 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
 50 55 60

 Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
 65 70 75 80

 Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
 85 90 95

 Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
 100 105 110

 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 115 120 125

Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 130 135 140
 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 145 150 155 160
 Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
 165 170 175
 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
 180 185 190
 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
 195 200 205
 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
 210 215 220
 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
 225 230 235 240
 Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
 245 250 255
 Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
 260 265 270
 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
 275 280 285
 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
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<210> 13

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<212> DNA

<213> Streptococcus agalactiae

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<222> (1)..(1011)

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Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
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aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
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Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
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ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca	240
Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro	
65 70 75 80	
gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca	288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
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Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu	
100 105 110	
aat ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt ttc aac act aac cac gat atc ctt gat gga act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt ctt gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct tta caa gac aac ttt ggt gtt aaa caa ggt ttg atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cac gca tac act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gca ggt gct gca aac atc gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	
cct aac tca act ggt gct gca aaa gct atc gga ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	

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 245 250 255
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 Glu Glu Val Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
 260 265 270
 tat act gaa gat cca atc gta tca tct gat atc gtt ggt att tca tac 864
 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr
 275 280 285
 ggt tca ttg ttt gat gct act caa act aaa gtt caa act gtt gac ggt 912
 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
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 Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
 305 310 315 320
 act tca caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa 1008
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<213> Streptococcus uberis
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<220>

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<222> (1)..(1011)

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Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly	
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Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro	
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 gaa aac att gac tgg gca act gac ggt gta gaa atc gtt ctt gaa gca	288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
 act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gct	336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Ala	
100 105 110	
 aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga gat gat gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val	
115 120 125	
 aaa act gtt gta ttt aac aca aac cat gac att ctt gac ggt aca gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
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Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
 gct aaa gct ttg caa gat aac ttt ggt gtt aaa caa ggt ttg atg aca	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
 act atc cac gct tac act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	

cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gca agc aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val	
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Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
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tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
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245 250 255	
gaa gaa atc aac gca gca atg aaa gca gct gca aac gat tca tac gga	816
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Asn Asp Ser Tyr Gly	
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Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr	
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Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
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aat caa tta gtt aaa gtt gtt tca tgg tat gac aac gaa atg tct tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gca caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa	1008
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<210> 16

<211> 336

<212> PRT

<213> Streptococcus uberis

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35 40 45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
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 Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
 65 70 75 80
 Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
 85 90 95
 Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Ala
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 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
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 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
 180 185 190
 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val
 195 200 205
 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
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 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
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 Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Glu Thr Ser Val
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 Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
 260 265 270
 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr
 275 280 285
 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
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 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
 20 25 30
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 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
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 Phe Asp Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
 65 70 75 80
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 Glu Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
 85 90 95
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 Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Glu
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 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 145 150 155 160
 gct aaa gct tta caa gat aac ttt ggc gta aaa caa ggt tta atg act 528
 Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
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cggt ggt ggt gac tta cgt cgt gcc cgt gct ggt gct aac aat att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val	
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cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cct gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
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tta aat ggt aaa ctt gac ggt gct gca caa cgt gta cca gtt cca aca	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
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Gly Ser Val Thr Glu Leu Val Ala Val Leu Asn Lys Glu Thr Ser Val	
245 250 255	
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Glu Glu Ile Asn Ser Val Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
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Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe	
275 280 285	
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Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
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<213> Streptococcus parauberis

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Glu Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
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Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Glu
 100 105 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
 115 120 125

Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 145 150 155 160

Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
 165 170 175

Thr Ile His Ala Tyr Thr Gly Asp Gln Met Leu Leu Asp Gly Pro His
 180 185 190

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val
 195 200 205

Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
 210 215 220

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
 225 230 235 240

Gly Ser Val Thr Glu Leu Val Ala Val Leu Asn Lys Glu Thr Ser Val
 245 250 255

Glu Glu Ile Asn Ser Val Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
 260 265 270

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe
 275 280 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
 290 295 300

Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
 305 310 315 320

Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
 325 330 335

<210> 19

<211> 1011

<212> DNA

<213> Streptococcus iniae

<220>

<221> CDS

<222> (1)..(1011)

<400> 19

atg gta gtt aaa gtt ggt att aac ggt ttc gga cgt atc ggt cgt ctt 48
 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
 1 5 10 15

gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc 96
 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
 20 25 30

aat gac ctt aca gat cct aac atg ctt gca cac ttg ttg aaa tat gat 144
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
 35 40 45

aca act caa ggt cgt ttt gac ggt aca gtt gaa gtt aaa gat ggt gga 192
 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
 50 55 60

ttc gaa gtt aac gga agc ttt gtt aaa gtt tct gca gaa cgc gaa cca 240
 Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 65 70 75 80

gca aac att gac tgg gct act gat ggt gta gac atc gtt ctt gaa gca 288
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
 85 90 95

aca ggt ttc ttc gct tct aaa gca gct gct gaa caa cac att cac gct 336
 Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
 100 105 110

aac ggt gcg aaa aaa gtt gtt atc aca gct cct ggt gga aat gac gtt 384
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 115 120 125

aaa aca gtt gtt tac aac act aac cat gat att ctt gat gga act gaa 432
 Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 130 135 140

aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gca tta caa gat aac ttt ggt gta aaa caa ggt tta atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cat ggt tac act ggt gac caa atg gtt ctt gac gga cca cac	576
Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gat ctt cgt cgt gct cgt gca gct gca gca aac atc gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val	
195 200 205	
cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gaa tta gta gca gtt ctt gaa aaa gat act tca gta	768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val	
245 250 255	
gaa gaa atc aat gca gct atg aaa gca gca gct aac gat tca tac ggt	816
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tac act gaa gat gct atc gta tca tca gat atc gta ggt att tct tac	864
Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr	
275 280 285	
ggt tca tta ttt gat gct act caa act aaa gta caa act gtt gat gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
290 295 300	
aat caa ttg gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gct caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

<210> 20

<211> 336

<212> PRT

<213> Streptococcus iniae

<400> 20

Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
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Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
65 70 75 80

Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
85 90 95

Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
100 105 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
115 120 125

Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175

Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His
180 185 190

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val
195 200 205

Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240

Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val
245 250 255

Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
260 265 270

Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr
 275 280 285
 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
 290 295 300
 Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
 305 310 315 320
 Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
 325 330 335

<210> 21

<211> 1347

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer Gap4
chimeric GapC protein

<220>

<221> CDS

<222> (1)..(1347)

<400> 21

atg aaa aaa ata aca ggg att att tta ttg ctt ctt gca gtc att att	48
Met Lys Lys Ile Thr Gly Ile Ile Leu Leu Leu Leu Ala Val Ile Ile	
1 5 10 15	
ctg tct gca tgc cag gca aac tac gga tcc ggt atg gta gtt aaa gtt	96
Leu Ser Ala Cys Gln Ala Asn Tyr Gly Ser Gly Met Val Val Lys Val	
20 25 30	
ggt att aac ggt ttc ggt cgt atc gga cgt ctt gca ttc cgt cgt att	144
Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala Phe Arg Arg Ile	
35 40 45	
caa aat gtt gaa ggt gtt gaa gta act cgt atc aac gac ctt aca gat	192
Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn Asp Leu Thr Asp	
50 55 60	
cca aac atg ctt gca cac ttg ttg aaa tac gat aca act caa gga cgt	240
Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp Thr Thr Gln Gly Arg	
65 70 75 80	
ttt gac gga act gtt gaa gtt aaa gaa ggt gga ttt gaa gta aac gga	288
Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe Glu Val Asn Gly	
85 90 95	
aac ttc atc aaa gtt tct gct gaa cgt gat cca gaa aac atc gac tgg	336
Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu Asn Ile Asp Trp	
100 105 110	

gca act gac ggt gtt gaa atc gtt ctg gaa gca ctc gag ggt act gta 384
 Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Leu Glu Gly Thr Val
 115 120 125

gaa gtt aaa gat ggt gga ttt gac gtt aac gga aaa ttc att aaa gtt 432
 Glu Val Lys Asp Gly Gly Phe Asp Val Asn Gly Lys Phe Ile Lys Val
 130 135 140

tct gct gaa aaa gat cca gaa caa att gac tgg gca act gac ggt gtt 480
 Ser Ala Glu Lys Asp Pro Glu Gln Ile Asp Trp Ala Thr Asp Gly Val
 145 150 155 160

gaa atc gtt ctt gaa atc gat ggt act gtt gaa gtt aaa gaa ggt gga 528
 Glu Ile Val Leu Glu Ile Asp Gly Thr Val Glu Val Lys Glu Gly Gly
 165 170 175

ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca 576
 Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 180 185 190

gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca 624
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
 195 200 205

act agt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct 672
 Thr Ser Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
 210 215 220

aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt 720
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 225 230 235 240

aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa 768
 Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 245 250 255

aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg 816
 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 260 265 270

gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act 864
 Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
 275 280 285

aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac 912
 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
 290 295 300

cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt 960
 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
 305 310 315 320

cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa	1008
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
325 330 335	
ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act	1056
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
340 345 350	
gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt	1104
Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val	
355 360 365	
gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt	1152
Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly	
370 375 380	
tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac	1200
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr	
385 390 395 400	
ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga	1248
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly	
405 410 415	
tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac	1296
Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
420 425 430	
act gct caa ctt gtt cgt aca ctt gag tat ttt gca aaa atc gct aaa	1344
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
435 440 445	
taa	1347

<210> 22

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GapC multiple epitope fusion protein

<400> 22

Met Lys Lys Ile Thr Gly Ile Ile Leu Leu Leu Leu Ala Val Ile Ile
1 5 10 15

Leu Ser Ala Cys Gln Ala Asn Tyr Gly Ser Gly Met Val Val Lys Val
20 25 30

Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala Phe Arg Arg Ile
35 40 45

Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn Asp Leu Thr Asp
 50 55 60
 Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp Thr Thr Gln Gly Arg
 65 70 75 80
 Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe Glu Val Asn Gly
 85 90 95
 Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu Asn Ile Asp Trp
 100 105 110
 Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Leu Glu Gly Thr Val
 115 120 125
 Glu Val Lys Asp Gly Gly Phe Asp Val Asn Gly Lys Phe Ile Lys Val
 130 135 140
 Ser Ala Glu Lys Asp Pro Glu Gln Ile Asp Trp Ala Thr Asp Gly Val
 145 150 155 160
 Glu Ile Val Leu Glu Ile Asp Gly Thr Val Glu Val Lys Glu Gly Gly
 165 170 175
 Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 180 185 190
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
 195 200 205
 Thr Ser Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
 210 215 220
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 225 230 235 240
 Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 245 250 255
 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 260 265 270
 Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
 275 280 285
 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
 290 295 300
 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
 305 310 315 320
 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
 325 330 335

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
 340 345 350

Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
 355 360 365

Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
 370 375 380

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
 385 390 395 400

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
 405 410 415

Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
 420 425 430

Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
 435 440 445